GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2006, 20:58:58 ; Search time 200 Seconds
                                             (without alignments)
                                             720.377 Million cell updates/sec

Title: US-10-604-944A-14
Perfect score: 77
Sequence: 1 ttaccctatagtgcagaaca..........aactttaaatgcatgggtaa 77

Scoring table: OLIGO_NUC
                   Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size :   18

Total number of hits satisfying chosen parameters: 211

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :   Issued_Patents_NA:*
                   1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                   2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                   3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                   4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                   5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                   6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                   7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                   8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                   9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                   10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	840	2	US-07-979-966A-1	Sequence 1, Appli
2	77	100.0	845	2	US-08-589-446-3	Sequence 3, Appli
3	77	100.0	845	2	US-08-444-882-3	Sequence 3, Appli
4	77	100.0	845	2	US-08-389-459A-3	Sequence 3, Appli
5	77	100.0	845	3	US-08-987-867A-3	Sequence 3, Appli
6	77	100.0	1314	3	US-08-392-794A-1	Sequence 1, Appli
7	77	100.0	2095	2	US-08-333-901-5	Sequence 5, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 11, 2006, 20:50:48 ; Search time 695 Seconds
                                         (without alignments)
                                         772.465 Million cell updates/sec

Title: US-10-604-944A-14
Perfect score: 77
Sequence: 1 ttaccctatagtgcagaaca..........aactttaaatgcatgggtaa 77

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size :   18

Total number of hits satisfying chosen parameters: 491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :   N_Geneseq_8:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	77	100.0	566	1	AAN71252	Aan71252 Sequence
2	77	100.0	630	6	ABK14492	Abk14492 Alpha Gal